Amendments to the Specification:

Please replace the paragraph beginning at page 10 line 14 with the following amended paragraph:

GAPN catalyses the irreversible oxidation of glyceraldehyde-3-phosphate and $NADP^+$ into 3-phosphoglycerate and NADPH. In most cells the conversion of glyceraldehyde-3-phosphate into 3-phosphoglycerate is only catalysed by the sequential action of two enzymes, i.e. NAD^+-dependent glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) and phosphoglycerate kinase (PGK) (EC 2.7.2.3) by conversion of NAD^+ and ADP into NADH and ATP ~~(see figure 1)~~. The net stoichiometry of the routes converting glyceralde-3-P into 3-P-glycerate are:

Please replace the paragraph beginning at page 14, line 5 with the following amended paragraph:

Construction of GAPN strain: gapN was expressed on a pYX212 2μ high-copy vector containing the URA3 gene and the TPI1 promoter. The plasmid was constructed directly in S. cerevisiae (M4054) by cotransformation and homologous recombination between EcoRI digested pYX212 and PCR-amplified gapN from *Streptococcus mutans*. PCR was performed on genomic DNA from *Streptococcus mutans* using Expand High Fidelity (Roche) and one primer identical to the TPI1promoter in pYX212 plus the first part of gapN (gapN-START-EcoRI-TPI promoter 5'-CTA CAA AAA ACA CAT ACA GGA ATT CAT GAC AAA ACA ATA TAA AAA TTA TG (SEQ ID NO 1)) and a second primer (gapN-STOP-NcoI-BamHI-AvrII-ApaI 5'-GGG CCC TAG GAT CCA TGG TGA ATT TTA TTA TTT GAT ATC AAA TAC GAC GG (SEQ ID NO 2)) identical to the MCS of pYX212 and the last part of gapN including the stop codon. Hence the ORF of *gapN* has been cloned between *EcoRI* and *NcoI* side in pYX212, down stream the *TPI1* promoter. The original start codon TTG was substituted with an ATG, to make translation in *S. cerevisiae* possible. Construction was verified by diagnostic PCR.

Please replace the paragraph beginning at page 17, line 10 with the following amended paragraph:

Example 4 Analysis of extracellular metabolites: Culture samples for determination of glucose, ethanol, glycerol, acetate, pyruvate and succinate concentrations were filtered through a 0.45 μm cellulose acetate filter (Osmonics) immediately after sampling, and the filtrate was frozen at -20°C until further analysis. The concentrations of the metabolites were determined by high-pressure liquid chromatography on an Aminex HPX-87Hm column (Bio-Rad) kept at 65°C and eluted at 0.6 ml per minute with 5 mM H_2SO_4. Acetate and pyruvate were detected spectrophotometrically by a Waters 486 Turnable Absobance Detector at 210 nm. Glucose, ethanol, glycerol and succinate were detected refractometrically by a Waters 410 Differential Refractometer. ~~Measurement of the metabolites during anaerobic fermentations is shown in Figure 3.~~ The final concentrations of the metabolites are listed below. It is seen that the GAPN strain produces more ethanol and less glycerol.

Please replace the paragraph beginning at page 20, line 10 with the following amended paragraph:

In order to verify that no mutations had occurred in the *gapN* encoding gene expressed in the 2μ high copy number plasmid, the part of the plasmid containing the *gapN* was sequenced. The sequence of the *gapN* as inserted into the plasmid and as found actually to be present therein was 'atg aca aaa caa tat aaa aat tat gtc aat ggc gag tgg aag ctt tca gaa aat gaa att aaa atc tac gaa ccg gcc agt gga gct gaa ttg ggt tca gtt cca gca atg agt act gaa gaa gta gat tat gtt tat gct tca gcc aag aaa gct caa cca gct tgg cga tca ctt tca tac ata gaa cgt gct gcc tac ctt cac aag gta gca gat att ttg atg cgt gat aaa gaa aaa ata ggt gct gtt ctt tcc aaa gag gtt gct aaa ggt tat aaa tca gca gtc agc gaa gtt gtt cgt act gca gaa atc att aat tat gca gct gaa gaa ggt ctt cgt atg gaa ggt gaa gtc ctt gaa ggc ggc agt ttt gaa gca gcc agc aag aaa aaa att gcc gtt gtt cgt cgt gaa cca gta ggt ctt gta tta gct att tca

cca ttt aac tac cct gtt aac ttg gca ggt tcg aaa att gca ccg gct ctt att gcg gga aat gtt att gct ttt aaa cca ccg acg caa gga tca atc tca ggg ctc tta ctt gct gaa gca ttt gct gaa gct gga ctt cct gca ggt gtc ttt aat acc att aca ggt cgt ggt tct gaa att gga gac tat att gta gaa cat caa gcc gtt aac ttt atc aat ttt act ggt tca aca gga att ggg gaa cgt att ggc aaa atg gct ggt atg cgt ccg att atg ctt gaa ctc ggt gga aaa gat tca gcc atc gtt ctt gaa gat gca gac ctt gaa ttg act gct aaa aat att att gca ggt gct ttt ggt tat tca ggt caa cgc tgt aca gca gtt aaa cgt gtt ctt gtg atg gaa agt gtt gct gat gaa ctg gtc gaa aaa atc cgt gaa aaa gtt ctt gca tta aca att ggt aat cca gaa gac gat gca gat att aca ccg ttg att gat aca aaa tca gct gat tat gta gaa ggt ctt att aat gat gcc aat gat aaa gga gcc act gcc ctt act gaa atc aaa cgt gaa ggt aat ctt atc tgt cca atc ctc ttt gat aag gta acg aca gat atg cgt ctt gct tgg gaa gaa cca ttt ggt cct gtt ctt ccg atc att cgt gtg aca tct gta gaa gaa gcc att gaa att tct aac aaa tcg gaa tat gga ctt cag gct tct atc ttt aca aat gat ttc cca cgc gct ttt ggt att gct gag cag ctt gaa gtt ggt aca gtt cat atc aat aat aag aca cag cgc ggc acg gac aac ttc cca ttc tta ggg gct aaa aaa tca ggt gca ggt att caa ggg gta aaa tat tct att gaa gct atg aca act gtt aaa tcc gtc gta ttt gat atc aaa' (SEQ ID NO 3), which is identical with the sequence of *gapN* from *Streptococcus mutans*.